CLAIMS

1. Method for testing, in a biological sample from a patient infected by HIV-2 containing at least one HIV-2 viral strain, the resistance of said HIV-2 viral strain to treatment with an antiprotease agent, wherein, using known methods, the presence of at least one mutation at one of positions 45, 54, 64, 84, and 90 of the protein sequence of the protease of said viral strain is investigated, said mutation having previously been found to elicit said resistance, and wherein, if such a mutation is found, it is concluded that a viral strain resistant to said antiprotease agent is present in the patient in question.

2. Method according to Claim 1, wherein:

a) using known methods, the presence of at least one mutation at one of said positions of the protein sequence of the protease of said viral strain in a biological sample taken from a patient infected with HIV-2 is investigated,

b) of the mutations founds in a), those which, after cloning in an HIV-2 virus, do not prevent the virus clone obtained from multiplying in culture in the presence of said antiprotease drug are selected, and

c) if at least one mutation is selected at step b), it is concluded that resistance exists to the antiprotease drug referred to in b).

3. Method according to Claim 1, wherein the presence of at least one mutation chosen from the following mutations:

K 45 R, I 54 M, I 64 V, I 84 L and L 90 M,

in the protein sequence of the protease of said viral strain is investigated and in which said resistance is concluded to exist if said mutation or said mutations is or are present.

Sub A11

4. Method according to any of the foregoing claims, wherein, to detect a mutation of the protein sequence of the protease, a corresponding mutation is sought in the nucleotide sequence of the gene of said protease.

5. Method according to Claim 4, wherein said test is carried out using hybridization techniques, according to known methods.

SUB C1

6. Method according to Claim 1, wherein said test is carried out using sequencing techniques, according to known methods.

7. Nucleotide probe usable in the method according to any one of Claims 1 to 5, comprising, as a minimum sequence, a sequence chosen from the group comprised of:

SUB A2

CCA AGA ATA for a mutated form of position 45.

CCA AGA GTA for a mutated form of position 45.

CCT AGA ATA for a mutated form of position 45.

TTT ATG AAC for a mutated form of position 54.

TTT ATG AAT for a mutated form of position 54.

GAA GTA AAA for a mutated form of position 64.

GAA GTA GAA for a mutated form of position 64.

AAC CTC TTT for a mutated form of position 84.

ATT ATG ACA for a mutated form of position 90.

ATC ATG ACA for a mutated form of position 90,

possibly supplemented by the nucleotide sequence of an adjacent region of the gene of said protease, on either side of the minimum sequence,

(b) a nucleotide sequence equivalent to a sequence defined in (a), and

(c) a sequence complementary to a sequence defined in (a) or in (b), said probe having a maximum of 40 nucleotides.

8. Method for testing, in a biological sample from a patient infected by HIV-2 containing at least one HIV-2 viral strain, the resistance of the HIV-2 viral strain to treatment with an antiprotease agent, wherein, using known methods, the presence of at least one mutation in position 10 or 46 of the protein sequence of the protease of said viral strain is investigated, said mutation having previously been found to elicit said resistance, and wherein, if such a mutation is found, it is concluded that a viral strain resistant to said antiprotease agent is present in the patient in question.

9. Method according to Claim 8, wherein:

a) using known methods, the presence of at least one mutation at one of said positions of the protein sequence of the protease of said viral strain in a biological sample taken from a patient infected with HIV-2 is investigated,

b) of the mutations founds in a), those which, after cloning in an HIV-2 virus, do not prevent the virus clone obtained from multiplying in culture in the presence of said antiprotease drug are selected, and

c) if at least one mutation is selected at step b), it is concluded that resistance exists to the antiprotease drug referred to in b).

10. Method according to Claim 8, wherein the presence of at least one mutation chosen from the following mutations:

V 10 I, I 46 V, and I 82 M

in the protein sequence of the protease of said viral strain is investigated and in which said resistance is concluded to exist if said mutation or said mutations is or are present.

11. Method according to any of Claims 8 to 10, wherein, to detect a mutation of the protein sequence of the protease, a corresponding mutation is sought in the nucleotide sequence of the gene of said protease.

SUB A3

12. Method according to Claim 11, wherein said test is carried out using sequencing techniques, according to known methods.

13. Method according to Claim 11, wherein said test is carried out using hybridization techniques, according to known methods.

14. Nucleotide probe usable in the method according to Claim 13, comprising, as a minimum sequence, a sequence chosen from the group comprised of:

(a) CCA ATA GTC for a mutated form of position 10.

AAA GTA GTA for a mutated form of position 46.

CCA ATG AAC for a mutated form of position 82.

possibly supplemented by the nucleotide sequence of an adjacent region of the gene of said protease, on either side of the minimum sequence,

(b) a nucleotide sequence equivalent to a sequence defined in (a), and

(c) a sequence complementary to a sequence defined in (a) or in (b) , said probe having a maximum of 40 nucleotides.

Add C2